

REMARKS

The amendment filed June 30, 2003 has been entered. Accordingly, claims 19-36 are pending. Claims 1-18 have been cancelled. Claims 19-36 have been previously submitted. Claim 19 is amended herein to recite a sequence identifier (SEQ ID NO: 9) for the cucumber expansin sequence cucumber Ex29 (GenBank Accession No. U30382). No issue of new matter is believed to be introduced by this amendment. Accordingly, claim 19, as amended, and claims 20-36 are presently under consideration.

The specification and abstract are amended herein, where appropriate, to include a sequence identifier (SEQ ID NO: 9) for the cucumber expansin sequence cucumber Ex29 (GenBank Accession No. U30382). No issue of new matter is believed to be introduced by this amendment.

A substitute Sequence Listing is submitted herein which presents the nucleic and amino acid sequences (SEQ ID NOs: 9 and 10) of the cucumber expansin sequence cucumber Ex29 (GenBank Accession No. U30382). No issue of new matter is believed to be introduced by this amendment.

The Examiner has indicated that the cancellation of the previously restricted claims and the submission of new claims has warranted issuance of a supplemental restriction.

The Examiner acknowledges that Applicants have elected with traverse the claims of Group I. It is the Examiner's position that Applicants did not elect a sequence in the amendment filed on June 30, 2003. Applicants would direct the Examiner's attention to page 7 (first paragraph) of the amendment filed June 30, 2003, wherein Applicants did elect a nucleic acid sequence of a particular species. Inasmuch as Applicants' amendment has warranted a supplemental restriction, Applicants assume that the Examiner is requiring Applicants to revisit the election in the context of the supplemental restriction. Accordingly, Applicants have elected herein a group as designated by the Examiner, and a particular expansin nucleic acid sequence and its species' source.

Applicants also note that the Examiner has objected to claim 1 for recitation of a sequence designated as Ex29, which requires an assigned sequence identifier. In that claim 1 has been cancelled, Applicants assume that the Examiner is actually referring to claim 19.

Accordingly, Applicants submit herewith a Substitute Sequence Listing wherein cucumber expansin sequence Ex29 (GenBank Accession No. U30382) is assigned a sequence identifier. Specifically, the nucleic acid sequence of cucumber expansin is identified as SEQ ID NO: 9 and the amino acid sequence encoded therefrom is identified as SEQ ID NO: 10. Applicants assert that the attached Substitute Sequence Listing does not comprise new matter because the GenBank Accession No. U30382 of cucumber expansin sequence Ex29 is specifically and repeatedly referred to throughout the specification. See, for example, page 18, last paragraph, wherein the GenBank Accession number for cucumber Ex29 (also known as Cs-EXP1) is presented and a reference detailing the identification of cucumber expansin cDNA clones (Shcheraban *et al.*) is cited. Moreover, Example 3 (pages 18-20), describes the construction of a transformation vector comprising cucumber Ex29 (Accession No. U30382) and its transfer into *Agrobacterium tumefaciens* strain EHA105. Example 4 (pages 20-22) further details transformation of plants with constructs comprising the cucumber Ex29 sequence and effects mediated thereby.

By this Office Action, the Examiner has required restriction to one of the following inventions under 35 U.S.C. §121:

- Group I. Claims 19-23, 31, and 34-36 drawn to a method of transforming trees to modify the fibre characteristics in trees comprising transforming said plant with any chimeric gene comprising a promoter operably linked to a nucleic acid sequence in sense orientation encoding an expansin capable of modifying at least one of: fibre cell wall extension, tree height or internode length, classified in class 800, subclass 290 for example.
- Group II. Claims 19 and 22, drawn to a method of transforming trees to modify the fibre characteristics in trees comprising transforming said plant with any chimeric gene comprising a promoter operably linked to a nucleic acid sequence in antisense orientation wherein said sequence is capable of modifying at least one of: fibre cell wall extension, tree height or internode length, classified in class 800, subclass 290 for example.
- Group III. Claims 24-30, and 32-33, drawn to a nucleic acid sequence and chimeric gene comprising said nucleic acid sequence, classified in class 536, subclass 23.1 for example.

Responsive to the Requirement for restriction, Applicants elect to prosecute the invention of Group I, with traverse, Claims 19-23, 31, and 34-36 drawn to a method of transforming trees to modify the fibre characteristics in trees comprising transforming said plant with any chimeric gene comprising a promoter operably linked to a nucleic acid sequence in sense orientation encoding an expansin capable of modifying at least one of: fibre cell wall extension, tree height or internode length, classified in class 800, subclass 290 for example.

Applicants respectfully request reconsideration of the Requirement for Restriction, or in the alternative, modification of the Restriction Requirement to allow prosecution of more than one group of Claims designated by the Examiner in the present Application, for the reasons provided as follows.

Under 35 U.S.C. §121 "two or more independent and distinct inventions ... in one Application may ... be restricted to one of the inventions." Inventions are "'independent'" if "there is no disclosed relationship between the two or more subjects disclosed" (MPEP 802.01). The term "'distinct'" means that "two or more subjects as disclosed are related ... but are capable of separate manufacture, use or sale as claimed, AND ARE PATENTABLE OVER EACH OTHER" (MPEP 802.01) (emphasis in original). However, even with patentably distinct inventions, restriction is not required unless one of the following reasons appear (MPEP 808.02):

1. Separate classification
2. Separate status in the art; or
3. Different field of search.

Further, under Patent Office Examining Procedures, "[i]f the Search and Examination of an entire Application can be made without serious burden, the Examiner must examine it on the merits, even though it includes claims to distinct or independent inventions" (MPEP 803, Rev. 8, May 1988) (emphasis added).

Applicants respectfully submit that the groups designated by the Examiner fail to define compositions and methods, with properties so distinct as to warrant separate Examination and Search. Claims 19 and 22 of Group II, drawn to a method of transforming trees to modify the fibre characteristics in trees comprising transforming said plant with any chimeric gene

comprising a promoter operably linked to a nucleic acid sequence in antisense orientation wherein said sequence is capable of modifying at least one of: fibre cell wall extension, tree height or internode length are fundamentally related to claims 19-23, 31, and 34-36 of Group I, drawn to a method of transforming trees to modify the fibre characteristics in trees comprising transforming said plant with any chimeric gene comprising a promoter operably linked to a nucleic acid sequence in sense orientation encoding an expansin capable of modifying at least one of: fibre cell wall extension, tree height or internode length. The search for any of the methods separately classified by the Examiner as the invention of Group II would require an additional search of the **identical** classes wherein the claims of Group I are classified, thus resulting in a duplicate search for the same material. Thus, Applicants submit that the Search and Examination of the entire Application, or, at least, of Group II with Group I can be made without serious burden, and therefore the Examiner should examine all of the claims of the Application on the merits.

Moreover, Applicants assert that the claims classified by the Examiner in Group I and II are universally directed to a method for transforming trees to modify fibre characteristics in trees, wherein the method comprises stably incorporating a chimeric gene comprising a promoter and a nucleic acid sequence encoding an expansin (SEQ ID NOs: 1-6 and 9, and parts thereof, and sequences substantially similar thereto and having the same function) capable of modifying at least one of: fibre cell wall extension, tree height or internode length, or a combination thereof; and regenerating a tree having an altered genome. The methods of claims 19-23, 31, and 34-36 are, therefore, clearly directed to the same invention in all aspects. The orientation of the sequence encoding the expansin capable of modifying the above characteristics does not alter the directive of the invention. The method of the invention and its objective are the same, irrespective of the orientation of the nucleic acid sequence encoding the expansin having such functional properties.

The Examiner's assertions to the contrary notwithstanding, Applicants respectfully submit that conjoint examination and inclusion of all of the Claims of the present Application would not present an undue burden on the Examiner, and accordingly, withdrawal of the

Requirement for Restriction, or, at the least, modification to include the Claims drawn to Group I and Group II is in order.

The Examiner has also indicated that for the election to be complete, an election of sequence is also required, along with an indication as to whether the sequence is derived from *Eucalyptus* or cucumber. Accordingly, Applicants elect SEQ ID NO: 9, the cucumber expansin nucleic acid sequence Ex29, with **traverse**.

Applicants assert that, in the context of the methods of the present invention, the nucleic acid sequences encoding an expansin are related to each other both structurally and functionally. It is well known that expansin nucleic acid sequences, even those derived from different species share a significant degree of homology. As stated in the instant specification:

Expansin cDNAs have been isolated and characterised from a number of plants and it is now evident that expansins exist as a multi-gene family showing a high level of conservation between species. cDNAs with high degrees of homology have been identified from collections of anonymous Expression Sequence Tag (EST) cDNAs from Arabidopsis and rice. These EST cDNAs exhibit a high degree of homology at the level of protein sequence (60-87%) indicating that expansin structure is highly conserved (Shcherban et al 1995).

See page 8, first paragraph. Moreover, the claims clearly indicate the functionality which is shared among the expansins and encompassed by the method of the invention. That is, the capability of modifying at least one of: fibre cell wall extension, tree height or internode length, or a combination thereof. In view of the above, Applicants respectfully request that the Examiner reconsider the requirement for the election of only a single nucleic acid sequence for continued prosecution in the present application. The conserved **structural** and **functional** characteristics of the expansins, such characteristics either known in the art or described in the present application, support Applicants' position that the use of any of SEQ ID NOs: 1-6 and 9 in the method of the invention fails to validate categorization as different inventions. Accordingly, Applicants respectfully request that the Examiner withdraw the requirement for the election of a

single species of nucleic acid sequence and examine the present claims as they may pertain to the use of any of SEQ ID NOs: 1-6 and 9.

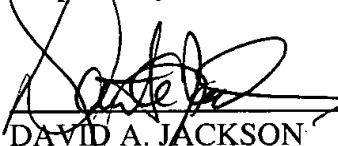
Fees

No additional fees are believed to be necessitated by the foregoing Response. However, should this be erroneous, authorization is hereby given to charge Deposit Account No. 11-1153 for any underpayment, or credit any overages.

Conclusions

In view of the above, withdrawal of the Requirement for the Restriction is requested, and an early action on the merits of the Claims is courteously solicited.

Respectfully submitted,


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Date: November 24, 2003

Enclosure: Substitute Sequence Listing
 Petition for One-Month Extension of Time